

SEQUENCE LISTING

<110> Dai, Ken-Shwo

<120> HUMAN RPS6KA6-RELATED GENE VARIANT ASSOCIATED WITH LUNG CANCERS

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<141> 2004-03-23

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<170> PatentIn version 3.1

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Lys	Pro	Ser	Asn	Ile	Leu 550	Tyr	Met	Asp	Glu	Ser 555	Ala	Ser	Ala	Asp	Ser 560		
atc	agg	ata	tgt	gat	ttt	ggg	ttt	gca	aaa	caa	ctt	cga	gga	gaa	aat	1728	
Ile	Arg	Ile	Cys	Asp	Phe	Gly	Phe	Ala	Lys	Gln	Leu	Arg	Gly	Glu	Asn		

565								570				575				
gga	ctt	ctc	tta	act	cca	tgc	tac	act	gca	aac	ttt	gtt	gca	cct	gag	1776
Gly	Leu	Leu	Leu	Thr	Pro	Cys	Tyr	Thr	Ala	Asn	Phe	Val	Ala	Pro	Glu	
			580					585					590			
gtt	ctt	atg	caa	cag	gga	tat	gat	gct	gct	tgt	gat	atc	tgg	agt	tta	1824
Val	Leu	Met	Gln	Gln	Gly	Tyr	Asp	Ala	Ala	Cys	Asp	Ile	Trp	Ser	Leu	
		595					600					605				
gga	gtc	ctt	ttt	tac	aca	atg	ttg	gct	ggc	tac	act	cca	ttt	gct	aat	1872
Gly	Val	Leu	Phe	Tyr	Thr	Met	Leu	Ala	Gly	Tyr	Thr	Pro	Phe	Ala	Asn	
	610					615					620					
ggc	ccc	aat	gat	act	cct	gaa	gag	ata	ctg	ctg	cgt	ata	ggc	aat	gga	1920
Gly	Pro	Asn	Asp	Thr	Pro	Glu	Glu	Ile	Leu	Leu	Arg	Ile	Gly	Asn	Gly	
	625				630					635					640	
aaa	ttc	tct	ttg	agt	ggg	gga	aac	tgg	gac	aat	att	tca	gac	gga	gca	1968
Lys	Phe	Ser	Leu	Ser	Gly	Gly	Asn	Trp	Asp	Asn	Ile	Ser	Asp	Gly	Ala	
				645					650					655		
aag	gat	ttg	ctt	tcc	cat	atg	ctt	cat	atg	gac	cca	cat	cag	cgg	tat	2016
Lys	Asp	Leu	Leu	Ser	His	Met	Leu	His	Met	Asp	Pro	His	Gln	Arg	Tyr	
			660					665					670			
act	gct	gaa	caa	ata	tta	aag	cac	tca	tgg	ata	act	cac	aga	gac	cag	2064
Thr	Ala	Glu	Gln	Ile	Leu	Lys	His	Ser	Trp	Ile	Thr	His	Arg	Asp	Gln	
		675					680					685				
ttg	cca	aat	gat	cag	cca	aag	aga	aat	gat	gtg	tca	cat	gtt	gtt	aag	2112
Leu	Pro	Asn	Asp	Gln	Pro	Lys	Arg	Asn	Asp	Val	Ser	His	Val	Val	Lys	
	690					695				700						
gga	gca	atg	gtt	gca	aca	tac	tct	gcc	ctg	act	cac	aag	acc	ttt	caa	2160
Gly	Ala	Met	Val	Ala	Thr	Tyr	Ser	Ala	Leu	Thr	His	Lys	Thr	Phe	Gln	
	705				710				715						720	
cca	gtc	cta	gag	cct	gta	gct	gct	tca	agc	tta	gcc	cag	cga	cgg	agc	2208
Pro	Val	Leu	Glu	Pro	Val	Ala	Ala	Ser	Ser	Leu	Ala	Gln	Arg	Arg	Ser	
			725					730					735			
atg	aaa	aag	cga	aca	tca	act	ggc	ctg								2235
Met	Lys	Lys	Arg	Thr	Ser	Thr	Gly	Leu								
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Val	Phe	Ser	Gly	Gly	Gly	Ala	Ser	Ser	Gly	Glu	Val	Asn	Gly	Leu	Lys
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Met Val Asp Glu Pro Met Glu Glu Gly Glu Ala Asp Ser Cys His Asp
 35 40 45

Glu Gly Val Val Lys Glu Ile Pro Ile Thr His His Val Lys Glu Gly
 50 55 60

Tyr Glu Lys Ala Asp Pro Ala Gln Phe Glu Leu Leu Lys Val Leu Gly
 65 70 75 80

Gln Gly Ser Phe Gly Lys Val Phe Leu Val Arg Lys Lys Thr Gly Pro
 85 90 95

Asp Ala Gly Gln Leu Tyr Ala Met Lys Val Leu Lys Lys Ala Ser Leu
 100 105 110

Lys Val Arg Asp Arg Val Arg Thr Lys Met Glu Arg Asp Ile Leu Val
 115 120 125

Glu Val Asn His Pro Phe Ile Val Lys Leu His Tyr Ala Phe Gln Thr
 130 135 140

Glu Gly Lys Leu Tyr Leu Ile Leu Asp Phe Leu Arg Gly Gly Asp Val
 145 150 155 160

Phe Thr Arg Leu Ser Lys Glu Val Leu Phe Thr Glu Glu Asp Val Lys
 165 170 175

Phe Tyr Leu Ala Glu Leu Ala Leu Ala Leu Asp His Leu His Gln Leu
 180 185 190

Gly Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu
 195 200 205

Ile Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Glu Ser Val
 210 215 220

Asp Gln Glu Lys Lys Ala Tyr Ser Phe Cys Gly Thr Val Glu Tyr Met
 225 230 235 240

Ala Pro Glu Val Val Asn Arg Arg Gly His Ser Gln Ser Ala Asp Trp
 245 250 255

Trp Ser Tyr Gly Val Leu Met Phe Glu Met Leu Thr Gly Thr Leu Pro
 260 265 270

Phe Gln Gly Lys Asp Arg Asn Glu Thr Met Asn Met Ile Leu Lys Ala
 275 280 285

Lys Leu Gly Met Pro Gln Phe Leu Ser Ala Glu Ala Gln Ser Leu Leu
 290 295 300

Arg Met Leu Phe Lys Arg Asn Pro Ala Asn Arg Leu Gly Ser Glu Gly
 305 310 315 320

Val Glu Glu Ile Lys Arg His Leu Phe Phe Ala Asn Ile Asp Trp Asp
 325 330 335

Lys Leu Tyr Lys Arg Glu Val Gln Pro Pro Phe Lys Pro Ala Ser Gly
 340 345 350

Lys Pro Asp Asp Thr Phe Cys Phe Asp Pro Glu Phe Thr Ala Lys Thr
 355 360 365

Pro Lys Asp Ser Pro Gly Leu Pro Ala Ser Ala Asn Ala His Gln Leu
 370 375 380

Phe Lys Gly Phe Ser Phe Val Ala Thr Ser Ile Ala Glu Glu Tyr Lys
 385 390 395 400

Ile Thr Pro Ile Thr Ser Ala Asn Val Leu Pro Ile Val Gln Ile Asn
 405 410 415

Gly Asn Ala Ala Gln Phe Gly Glu Val Tyr Glu Leu Lys Glu Asp Ile
 420 425 430

Gly Val Gly Ser Tyr Ser Val Cys Lys Arg Cys Ile His Ala Thr Thr
 435 440 445

Asn Met Glu Phe Ala Val Lys Ile Ile Asp Lys Ser Lys Arg Asp Pro
 450 455 460

Ser Glu Glu Ile Glu Ile Leu Met Arg Tyr Gly Gln His Pro Asn Ile
 465 470 475 480

Ile Thr Leu Lys Asp Val Phe Asp Asp Gly Arg Tyr Val Tyr Leu Val
 485 490 495

Thr Asp Leu Met Lys Gly Gly Glu Leu Leu Asp Arg Ile Leu Lys Gln
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Lys Cys Phe Ser Glu Arg Glu Ala Ser Asp Ile Leu Tyr Val Ile Ser

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Lys	Thr	Val	Asp	Tyr	Leu	His	Cys	Gln	Gly	Val	Val	His	Arg	Asp	Leu
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Lys	Pro	Ser	Asn	Ile	Leu	Tyr	Met	Asp	Glu	Ser	Ala	Ser	Ala	Asp	Ser
545					550					555					560
Ile	Arg	Ile	Cys	Asp	Phe	Gly	Phe	Ala	Lys	Gln	Leu	Arg	Gly	Glu	Asn
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Gly	Leu	Leu	Leu	Thr	Pro	Cys	Tyr	Thr	Ala	Asn	Phe	Val	Ala	Pro	Glu
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Gly	Pro	Asn	Asp	Thr	Pro	Glu	Glu	Ile	Leu	Leu	Arg	Ile	Gly	Asn	Gly
625					630					635					640
Lys	Phe	Ser	Leu	Ser	Gly	Gly	Asn	Trp	Asp	Asn	Ile	Ser	Asp	Gly	Ala
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Lys	Asp	Leu	Leu	Ser	His	Met	Leu	His	Met	Asp	Pro	His	Gln	Arg	Tyr
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Thr	Ala	Glu	Gln	Ile	Leu	Lys	His	Ser	Trp	Ile	Thr	His	Arg	Asp	Gln
	675						680					685			
Leu	Pro	Asn	Asp	Gln	Pro	Lys	Arg	Asn	Asp	Val	Ser	His	Val	Val	Lys
	690					695					700				
Gly	Ala	Met	Val	Ala	Thr	Tyr	Ser	Ala	Leu	Thr	His	Lys	Thr	Phe	Gln
705					710					715					720
Pro	Val	Leu	Glu	Pro	Val	Ala	Ala	Ser	Ser	Leu	Ala	Gln	Arg	Arg	Ser
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